From:	Jay Field
To:	Eric Blischke/R10/USEPA/US@EPA
Cc:	Robert Gensemer; Burt Shephard/R10/USEPA/US@EPA; Chip Humphrey/R10/USEPA/US@EPA; Joe Goulet/R10/USEPA/US@EPA; Robert Neely
Subject:	Re: Summary of Sediment Bioassay Interpretation Resolution
Date:	07/14/2009 01:35 PM

Eric,
my understanding was that unlike the round 2 data, the round 3 represented re-testing of the same sediment so that there were results for each of the 2 batches of R3 tox tests. If the R3 "replicate" samples were actually 100 ft apart, then not averaging is appropriate as Bob states. note that the R2 6 stations with samples collected 100 ft apart were labelled differently and several of those field replicates are included as separate samples in the ref envelope.
Jay

Robert Gensemer wrote:

> Eric: I don't think anyone is suggesting that we average the upstream samples with the three samples per location. I don't exactly know what is different about G788, but I assume the a/b samples were splits from the same physical sample? I would average the latter, but not the former.
> -Bob
>
> -----Original Message-----
> From: Blischke.Eric@epamail.epa.gov
> [mailto:Blischke.Eric@epamail.epa.gov]
> Sent: Tuesday, July 14, 2009 12:26 PM
> To: Jay Field
> Cc: Shephard.Burt@epamail.epa.gov; Humphrey.Chip@epamail.epa.gov; Goulet.Joe@epamail.epa.gov; Robert Gensemer; Robert Neely
> Subject: Re: Summary of Sediment Bioassay Interpretation Resolution
>
> When we designed the original upstream sampling program, we identified
> six locations and collected three samples at each location. However,
> the samples were collected some distance (~100') apart as I recall.
> Given this fact, would we really be introducing bias by including the
> duplicate? Would it really matter if we collected three or four samples
> from a given location? Your argument assumes that the duplicates have
> the same characteristics beyond the similar characteristics of each of
> the six locations or the upstream area in general.
>
> Eric
>
> Jay Field <Jay.Field@noaa.gov>
> 07/14/2009 12:17 PM
>
> To
> Eric Blischke/R10/USEPA/US@EPA
> cc
> Robert Gensemer <rgensemer@parametrix.com>, Burt Shephard/R10/USEPA/US@EPA, Chip Humphrey/R10/USEPA/US@EPA,

Joe

Goulet/R10/USEPA/US@EPA,

Robert

Neely

<Robert.Neely@noaa.gov>

Subject

Re: Summary of Sediment

Bioassay

Interpretation Resolution

Eric,
Regarding number 4): It does matter, since it gives more weight
to two
of the stations in the reference envelope. You could include both
but
give them a weight of 1/2, if your curve fitting package allows
weighting. Helping the curve fitting procedure is kind of
irrelevant if

the distribution is skewed by including two samples twice.
Jay

Blischke.Eric@epamail.epa.gov wrote:

> Bob, thanks for the quick response. I have a few
> questions/comments:
>
> Regarding number 2), do we understand why the biomass
> values don't
> match. If the control normalization was done correctly
> and there were
> no reporting errors,could there be a difference in how
> total biomass

was

> reported?
> Regarding number 3), I will make sure that I specify
> survivorship in

my

> email.
> Regarding number 4), it seems we did not specify whether
> to pool or to
> handle to duplicates as individual sample results when
> calculating the
> reference envelope. My question is two-fold - 1) does
> it matter? and

2)

> if we include the duplicates as individual samples,
> could this help

our

curve fitting procedure because we now have an additional one or two
samples?
Regarding number 6) Burt and I discussed this. He seemed to think

that

it is more valid statistically to fit the entire curve rather than the
lower end due to the small number of samples at the lower end of the
distribution. My original thought was along the lines of yours but

Burt

convinced me otherwise. We can revisit this though.

Once I get some additional feedback, I will finalize the email and

send

to John Toll and Bob Wyatt.

Thanks, Eric

Robert Gensemer

<rgensemer@param

etrix.com>

To

Eric
Blischke/R10/USEPA/US@EPA,

07/13/2009 08:34   Burt
Shephard/R10/USEPA/US@EPA,

PM
"jay.field@noaa.gov"

<jay.field@noaa.gov>, Joe

Goulet/R10/USEPA/US@EPA

cc

Chip
Humphrey/R10/USEPA/US@EPA

Subject

RE: Summary of
Sediment Bioassay

Interpretation
Resolution

Eric: A few observations from my perspective:

2) The control-normalization looks correct for biomass, but if I

recall

(I don't have my files with me at the moment) that LWG's biomass

values

for individual stations did not quite match values that Jay derived

for

table RE-1.
3) You have the control normalization correct (test/control) but we

need

to be careful to recommend use of survivorship, not mortality, to be fully consistent with our guidance and numeric examples. I realize

Table

2-1 used mortality, but we have been very consistent all along that we need to use survivorship, and from a recent call with Burt, Don McD. agrees that control-normalized survivorship is the correct value to

use,

not ctrl-norm mortality. Yes, they relate directly (or should I say, inversely) to one another, but the 5th percentile calculation could be different using one vs. the other, so we need to be consistent, and

use

survivorship.
4) I could not find any explicit guidance regarding the duplicate RE samples. Its not in the McDonald report that I can find, and I don't think we went into this level of detail in the problem formulation. It may be one of those things that just seemed very obvious to all of us, and so never felt the need to explicitely direct it. Actually, it may have only come up, to my recollection, during our own RE calculations

in

March. So table RE-1 definitely reflects this approach, although I

don't

think it was spelled out in the text.
6) I agree with your summary here, except to say that we need to not
just chose the best overall curve fit, but particularly in the case of
Hyalella biomass, we need a curve that fits the lower tail (i.e., 5th
%ile) of the distribution best. For the other three endpoints, this is
probably not an issue (i.e., best fit is also best 5th %ile fit). But
for Hyl biomass, we need to think more carefully about what

distribution

fits at the lower tail of the distribution. I think this is a valid
approach that makes the best out of the available data. LWG's curve

fit

created a 5th %ile value that was quite a bit lower than the empirical
numbers; I do not think that was the most appropriate representation

of

the data.

Bob

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þ Before printing, please think green.

From: Blischke.Eric@epamail.epa.gov
[Blischke.Eric@epamail.epa.gov]
Sent: Monday, July 13, 2009 5:02 PM
To: Robert Gensemer; Shephard.Burt@epamail.epa.gov;

jay.field@noaa.gov;

Goulet.Joe@epamail.epa.gov

Cc: Humphrey.Chip@epamail.epa.gov
Subject: Summary of Sediment Bioassay Interpretation Resolution

As you are aware, we have been discussing some of the details of the LWG's interpretation of the Portland Harbor sediment bioassay results. Some elements of the interpretation were discussed during a conference call on Thursday, June 18, 2009.

Here is where I believe we are:

1) No transcription errors were identified during a review of the reference envelope bioassay results.
2) The total biomass calculations were done correctly.
3) Mortality should be computed as test/control. This is consistent with Table 2-1 in the March 17, 2006 Bioassay Interpretation Report, ASTM Method E-1706, and EPA Guidance.
4) Duplicate reference envelope samples should be pooled (averaged) rather than treated as individual samples. This is consistent with February 15, 2008 problem formulation (Note: is this the correct reference? I could not find this in either the problem formulation

nor

the MacDonald benthic risk evaluation)
5) Identification of Level 1, Level 2 and Level 3 thresholds: The toxicity thresholds should be calculated based on 10% of the reference envelope not an absolute 10%. This is consistent with Tables RE 1,

RE-2

and the text of EPA's March 31, 2009 direction on the Calculation and Use of Reference Envelope for Portland Harbor Sediment Toxicity Test Interpretation
6) Identification of the 5% of the reference envelope should be accomplished using a range of curve fitting procedures appropriate for the data set distribution. The curve fitting procedure with the best overall fit should be selected and the 5% calculated using the best

fit

curve fitting procedure.

The above procedures for computing the results of the bioassay tests, calculating hit/no-hit designations, developing the reference envelope and identifying Level 1, Level 2 and Level 3 toxicity hits should be followed.

Please look this over and make sure it matches up with the recommended procedures. See also my note about the pooling of the reference duplicate samples. Once everyone agrees with the outlined procedures,

I

will send an email to the LWG summarizing this and recommending a conference call to discuss if there area any questions.

Thanks, Eric

--
Jay Field
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